

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 18:08:26 ; Search time 82 seconds

(without alignments)
892.033 Million cell updates/sec

Title: US-09-922-895-1

Perfect score: 1854
Sequence: 1 MTSLSDTVEFTGTTSYDDY.....LERTSVSPSTAPELSIYF 355

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMEL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1710	92.2	355	6	Q8WMR4
2	1709	92.2	355	6	Q8WMR5
3	1704	91.9	355	6	Q9BDS8
4	1376.5	74.2	358	6	Q9NOM0
5	1148	61.9	351	6	Q9MYU9
6	1128.5	60.9	355	6	Q9MYU8
7	1115.5	60.2	355	11	Q9JLY8
8	1115.5	60.2	355	11	Q9JLY9
9	958.5	51.7	383	12	Q89609
10	958	51.7	339	6	Q9TUS3
11	956	51.6	339	6	Q9TUS0
12	953.5	51.4	352	6	Q9SNC6
13	953.5	51.4	352	6	Q9TUS4
14	953	51.4	339	6	Q9TUS4
15	952.5	51.4	352	6	Q9TUS4
16	952	51.3	339	6	Q9TUS3

17	952	51.3	339	6	Q9TUS1	Q9TUS1 lemur varie
18	947.5	51.1	352	6	Q9TSK1	Q9TSK1 cercopithec
19	947.5	51.1	352	6	Q9TVA2	Q9TVA2 cercopithec
20	947.5	51.1	352	6	Q9SNC5	Q9SNC5 hylobates s
21	947.5	51.1	352	6	Q9SNC5	Q9SNC5 hylobates m
22	946.5	51.1	352	6	Q9TVA9	Q9TVA9 cercocobus
23	945.5	51.0	352	6	Q9TVA9	Q9TVA9 cercocobus
24	944.5	50.9	352	6	Q9TVA9	Q9TVA9 cercocobus
25	944.5	50.9	352	6	Q9SNE8	Q9SNE8 pan troglod
26	944.5	50.9	352	6	Q9SNE8	Q9SNE8 pan troglod
27	943.5	50.9	352	6	Q9TUS1	Q9TUS1 cercopithec
28	943.5	50.9	352	6	Q9SND0	Q9SND0 erythrocebu
29	942.5	50.8	352	6	Q9SNC5	Q9SNC5 cercopithec
30	942.5	50.8	352	6	Q9SND1	Q9SND1 mandrillus
31	942.5	50.8	352	6	Q9SNC7	Q9SNC7 nasalis lar
32	941.5	50.8	339	6	Q9TSN3	Q9TSN3 macaca fasc
33	941.5	50.8	352	6	Q9SNC1	Q9SNC1 macaca fasc
34	941.5	50.8	352	6	Q9SNC8	Q9SNC8 colobus pol
35	941.5	50.8	352	6	Q9SNC1	Q9SNC1 theopithec
36	940.5	50.7	352	6	Q9SNC2	Q9SNC2 mandrillus
37	940.5	50.7	352	6	Q9SNC3	Q9SNC3 miopithecus
38	940.5	50.7	352	6	Q9SNC2	Q9SNC2 calliochus
39	940.5	50.7	352	6	Q9TUS1	Q9TUS1 pygathrix a
40	939.5	50.7	339	6	Q9TUS1	Q9TUS1 macaca mulia
41	939.5	50.7	352	6	Q9TVA3	Q9TVA3 cercopithec
42	939.5	50.7	352	6	Q9TVA3	Q9TVA3 cercopithec
43	939.5	50.7	352	6	Q9TVA3	Q9TVA3 cercopithec
44	938.5	50.6	352	6	Q9TVA3	Q9TVA3 pan troglod
45	938.5	50.6	352	6	Q9TVA3	Q9TVA3 papio anubis

ALIGNMENTS

RESULT 1

Q8WMR4 PRELIMINARY; PRT; 355 AA.
AC Q8WMR4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chemokine receptor 3.
GN CCR3.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Iino T., Chu D., Sugimoto H., Kannan Y., Watanabe A., Liu N.,
RA Bacon K.B.;
RT "Cloning and characterization of cynomolgus monkey CCR3."
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY065647; AAL55443.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECPT_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G-PROTEIN_RECPT_FL_2; 1.
KW Receptor.
SO SEQUENCE 355 AA; 40793 MW; F3228C6835A1A830 CRC64;

Query Match 92.2% Score 1710; DB 6; Length 355;
Best Local Similarity 91.8% Pred. No. 7.8e-143;
Matches 326; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MTSLSDTVEFTGTTSYDDYGLCEKADTRALMQFPPPLSLVFTVGLGNVVVWILI 60
Db 1 MTSLSDTVEFTGTTSYDDYGLCEKADTRALMQFPPPLSLVFTVGLGNVVVWILI 60
Qy 61 KYRRLRTMTNTYLLNLALISDLFLVTLTPFWIHYRGHNWFGKCKLLSGFTGLXSE 120
|||||

ID	Q8MWR5	PRELIMINARY	PRT	355 AA
Db	61	KYRRIRIMTNTYLLNLMAISDLLEPTLPFWIMHYERBRMNVFSHGMOCKVLSGYHNTGLYSE	120	
QY	121	IFFIILLIDRYLAIVHAVPALRATVFGVTSIVTWGLATVALAPEIFETEELFEE	180	
Db	121	IFFIILLIDRYLAIVHAVPALRATVFGVTSIVTWGLATVALAPEIFETEELFEE	180	
QY	181	TLCsALYEDPNVYSRHFHTLMTJFCVLPLTVMAICTGTITKTLRCPSSKKYAIRL	240	
Db	181	TLCsALYEDPNVYSRHFHTLMTJFCVLPLTVMAICTGTITKTLRCPSSKKYAIRL	240	
QY	241	IFVIMAVFIFWTPYNAVALLSYOSIDFEGNDCERSKHLIDVLMVLEYEIVASHCCANPYI	300	
Db	241	IFVIMAVFIFWTPYNAVALLSYOSIDFEGNDCERSKHLIDVLMVLEYEIVASHCCANPYI	300	
QY	301	YAFGERRKRKYLRFHFHRLMLHLGRYIPFLPSKLERSSVSPSTAEPESLIVF	355	
Db	301	YAFGERRKRKYLRFHFHRLMLHLGRYIPFLPSKLERSSVSPSTAEPESLIVF	355	

ID	Q8MWR5	PRELIMINARY	PRT	355 AA
AC	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Chemokine receptor 3.			
GN	CCR3.			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OC	Cercopitheciinae; Macaca.			
OX	NCBI_TaxID=9541;			
XM	[1]			
RA	SEQUENCE FROM N.A.			
RA	Iino T., Chu D., Sugimoto H., Kannan Y., Watanabe A., Liu N.,			
RA	Bacon K.B.;			
RT	"Cloning and characterization of cynomolgus monkey CCR3."			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY065646; AAL55442.1; .			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7cm_1; 1.			
DR	PRINTS; PRO0037; GPCRHHODPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECIP_FL1; UNKNOWN.1.			
DR	PROSITE; PS50262; G_PROTEIN_RECIP_FL2; 1.			
KW	Receptor.			
SO	SEQUENCE			
QY	355 AA; 40779 MW; 32EBBDE21D032201 CRC64;			
QY	Query Match	92.2%; Score 1709; DB 6; Length 355;		
QY	Best Local Similarity	91.5%; Pred No. 9, 6e-143;		
QY	Matches	325; Conservative 13; Mismatches 17; Indels 0; Gaps 0		
QY	1	MTSLDLYETFGTSTYDDVGLCEKADTRALMAQFVPEPLSLVFTVGLGNVVMIL	60	
Db	1	MTSLDLYETFGTSTYDDVGLCEKADTRALMAQFVPEPLSLVFTVGLGNVVMIL	60	
QY	61	KYRRIRIMTNTYLLNLMAISDLLEPTLPFWIMHYERBRMNVFSHGMOCKVLSGYHNTGLYSE	120	
Db	61	KYRRIRIMTNTYLLNLMAISDLLEPTLPFWIMHYERBRMNVFSHGMOCKVLSGYHNTGLYSE	120	
QY	121	IFFIILLIDRYLAIVHAVPALRATVFGVTSIVTWGLATVALAPEIFETEELFEE	180	
Db	121	IFFIILLIDRYLAIVHAVPALRATVFGVTSIVTWGLATVALAPEIFETEELFEE	180	
QY	181	TLCsALYEDPNVYSRHFHTLMTJFCVLPLTVMAICTGTITKTLRCPSSKKYAIRL	240	
Db	181	TLCsALYEDPNVYSRHFHTLMTJFCVLPLTVMAICTGTITKTLRCPSSKKYAIRL	240	
QY	241	IFVIMAVFIFWTPYNAVALLSYOSIDFEGNDCERSKHLIDVLMVLEYEIVASHCCANPYI	300	
Db	241	IFVIMAVFIFWTPYNAVALLSYOSIDFEGNDCERSKHLIDVLMVLEYEIVASHCCANPYI	300	
QY	301	YAFGERRKRKYLRFHFHRLMLHLGRYIPFLPSKLERSSVSPSTAEPESLIVF	355	
Db	301	YAFGERRKRKYLRFHFHRLMLHLGRYIPFLPSKLERSSVSPSTAEPESLIVF	355	

ID	Q9BDS8	PRELIMINARY:	PRT:	355 AA.
DB	301 YAFGERRKTYLRFHFRHVLMLHCKYIFLPSEKLERISSVSPSTAEPELSIVF			355
RESULT 3				
ID	Q9BDS8	PRELIMINARY:	PRT:	355 AA.
AC	Q9BDS8:			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DR	01-OCT-2000 (TREMBLrel. 17, Last sequence update)			
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Cercopithecoidea; Macaca.			
NCBI_TaxID	9541;			
SEQUENCE FROM N.A.				
RP	MEDLINE-21134756; PubMed-11242524;			
RX	Wade-Evans A.M., Russell J., Jenkins A., Javan C.,			
RT	"Cloning and sequencing of cynomolgus macaque ccr3, gp15, and str133:			
RL	Potential coreceptors for HIV type 1, HIV type 2, and STV.*"			
DR	AIDS Res. Hum. Retroviruses 17:371-375(2001).			
DR	EMBL: AF291668; AAK25739.1; -.			
DR	HSSP: P02699; 1P88			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm_1; 1.			
DR	PRINTS: PR00237; GPCR_RHODOPSN.			
DR	PROSITE: PS00237; G_PROTEIN_RECPEP_F1_1; UNKNOWN_1.			
DR	PROSITE: PS50262; G_PROTEIN_RECPEP_F1_2; 1.			
DR	Receptor			
SV	SEQUENCE 355 AA: 40914 MW; 287865A177D26ICE CRC64;			
Query Match	91.9%; Score 1704; DB 6; Length 355;			
Best Local Similarity	91.8%; Pred. No. 2,6e-142;			
Matches 326; Conservative 12; Mismatches 17; Indels 0; Gaps 0				
QY	1 MTSIDVVEFGTSTSYDDVGLCEKADTRALMAQFVPPPLYSLVFTVGLGNVVVMMILI	60		
DB	1 MTSIDVVEFGTSTSYDDVGLCEKADTRALMAQFVPPPLYSLVFTVGLGNVVVMMILI	60		
QY	61 KYRRIRIMNTIYLLMLATSDILEFLVTLPPWHYVHGNNVFEHGCKILSGEYHNGLYSE	120		
DB	61 KYRRIRIMNTIYLLMLATSDILEFLVTLPPWHYVHGNNVFEHGCKILSGEYHNGLYSE	120		
QY	121 IFFIILLIDRLATVAVHAFARLARTVTEGVITSYTWGLAVLALPEFIYFETELFEE	180		
DB	121 IFFIILLIDRLATVAVHAFARLARTVTEGVITSYTWGLAVLALPEFIYFETELFEE	180		
QY	181 TLCSALYEDDYVYSRNRHETLMTFCGLVPLPLVMAICTYGIKTLRCPSKKRYAIRL	240		
DB	181 TLCSALYEDDYVYSRNRHETLMTFCGLVPLPLVMAICTYGIKTLRCPSKKRYAIRL	240		
QY	241 IFVIMAVFEIETPPVNAVAILSSYOSILFNGCCERSKHLDVLMVTEVLAASHCCNRYI	300		
DB	241 IFVIMAVFEIETPPVNAVAILSSYOSILFNGCCERSKHLDVLMVTEVLAASHCCNRYI	300		
QY	301 YAFVGERRKTYLRFHFRHVLMLHCKYIFLPSEKLERISSVSPSTAEPELSIVF	355		
DB	301 YAFVGERRKTYLRFHFRHVLMLHCKYIFLPSEKLERISSVSPSTAEPELSIVF	355		
RESULT 4				
ID	Q9NOMO	PRELIMINARY:	PRT:	358 AA.
AC	Q9NOMO:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DR	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DE	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	CCR3 receptor.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Wolfe G.C., Mudgett J.S.;
RT "Cloning and characterization of the sheep CCR3 receptor."
RL Submitted (May-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF266468; AAF71786.1; -
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 358 AA; 40985 MW; 2B54F9128590181E CRC64;

Query Match 74.28; Score 1376.5; DB 6; Length 358;
Best Local Similarity 73.38; Pred. No. 2e-113;
Matches 263; Conservative 41; Mismatches 50; Indels 5; Gaps 2;

QY 1 MTSLSLDTVEFETGTSYDDVGLCEKADTRALMAQFVPPYSLVFTVGLGNVNVV 56
DB 1 MANSVQGIETVGEVAGTTPYDYGALPCEKSNVKELAAQFLPPLSLVFMIGLGNVNV 60
QY 57 MIILKRLRIKNTIYLNLAIISDLFLVTLPMIHYRGHNWFGHGCKLLSGFYHTG 116
DB 61 VILTKKRLRIKNTIYLNLAIISDLFLVTLPMIHYRGHNWFGHGCKLLSGFYHTG 120
QY 117 LYEIIFILLTDRYLAIVHAFALRAFTVGVTSIYTWGLAVLAALPEFETEE 176
DB 121 LYEIIFILLTDRYLAIVHAFALRAFTVGVTSIYTWGLAVLAALPEFETEE 180
QY 177 LFEETLCSALYPEDTVYSNRHFTLRMTIFCLVPLLVMAICYTGIIKTLRCPSKRYK 236
DB 181 EAGLTICSPLYPENNVAMKQFALRNIIIGLALPLLVMAVCYSGIIKTLRCPSKRYK 240
QY 237 AILILFIVMAVFETFPYVAVALLISYOSILFGNDCERKHLDMVLTVEVLAISGCM 296
DB 241 AILILFIVMAVFETFPYVAVALLISYOSILFGNDCERKHLDMVLTVEVLAISGCM 299
QY 297 NPVIYAVGGRFRKYLHFFRHLLMHGRIYIPLPSEKLEERTSVSPSTAEPESLIVE 355
DB 300 NPVIYAVGGRFRKYLHFFRHLLMHGRIYIPLPSEKLEERTSVSPSTAEPESLIVE 358

RESULT 5
Q9MYJ9 PRELIMINARY; PRT; 351 AA.
ID Q9MYJ9
AC Q9MYJ9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chemokine receptor.
DE CCR1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
RA Ghanam A., Kretscher P.J., Pu H., Dunning L., Snider R.M.,
RA Morrissey M.M., Hesselgeser J., Perez H.D., Horuk R.;
RT "Species selectivity of a small molecule antagonist for the CCR1
RT chemokine receptor."
RL Eur. J. Pharmacol. 389:41-49(2000).
DR EMBL: AF127527; AAF36452.1; -
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS00237; GPCRHHODOPS.

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DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 351 AA; 40534 MW; B3FED6117A141552 CRC64;

Query Match 61.98; Score 1148; DB 6; Length 351;
Best Local Similarity 62.18; Pred. No. 2.7e-93;
Matches 221; Conservative 54; Mismatches 75; Indels 6; Gaps 3;

QY 1 MTSLSLDTVEFETGTSYDDVGLCEKADTRALMAQFVPPYSLVFTVGLGNVNVV 59
DB 1 MTSLSLDTVEFETGTSYDDVGLCEKADTRALMAQFVPPYSLVFTVGLGNVNVV 59
QY 60 IKYRLRIKNTIYLNLAIISDLFLVTLPMIHYRGHNWFGHGCKLLSGFYHTG 119
DB 60 IKYRLRIKNTIYLNLAIISDLFLVTLPMIHYRGHNWFGHGCKLLSGFYHTG 119
QY 120 EEIFILLTDRYLAIVHAFALRAFTVGVTSIYTWGLAVLAALPEFETEE 179
DB 120 EEIFILLTDRYLAIVHAFALRAFTVGVTSIYTWGLAVLAALPEFETEE 179
QY 180 ETLCALYPEDTVYSNRHFTLRMTIFCLVPLLVMAICYTGIIKTLRCPSKRYK 239
DB 180 HYSCLHFPESHKQWFOFQALKNIGLVPLLVMAVCYTGIIQILRRNKKSAVR 239
QY 240 LIFVIMAVFETFPYVAVALLISYOSILFGNDCERKHLDMVLTVEVLAISGCM 299
DB 240 LIFVIMAVFETFPYVAVALLISYOSILFGNDCERKHLDMVLTVEVLAISGCM 299
QY 300 IYAVGGRFRKYLHFFRHLLMHGRIYIPLPSEKLEERTSVSPSTAEPESLIVE 355
DB 300 IYAVGGRFRKYLHFFRHLLMHGRIYIPLPSEKLEERTSVSPSTAEPESLIVE 355

RESULT 6
Q9MYJ8 PRELIMINARY; PRT; 355 AA.
ID Q9MYJ8
AC Q9MYJ8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chemokine receptor.
DE CCR1.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
RA Ghanam A., Kretscher P.J., Pu H., Dunning L., Snider R.M.,
RA Morrissey M.M., Hesselgeser J., Perez H.D., Horuk R.;
RT "Species selectivity of a small molecule antagonist for the CCR1
RT chemokine receptor."
RL Eur. J. Pharmacol. 389:41-49(2000).
DR EMBL: AF127528; AAF36453.1; -
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; GPCRHHODOPS.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 355 AA; 40928 MW; 2B01C47E9874A2C1 CRC64;

Query Match 60.98; Score 1128.5; DB 6; Length 355;
Best Local Similarity 60.68; Pred. No. 1.4e-91;
Matches 215; Conservative 56; Mismatches 77; Indels 7; Gaps 1;

QY 8 VEEGTSYDDV-----GLCEKADTRALMAQFVPPYSLVFTVGLGNVNVV 60
DB 1 MTSLSLDTVEFETGTSYDDVGLCEKADTRALMAQFVPPYSLVFTVGLGNVNVV 60
QY 61 KYRLRIKNTIYLNLAIISDLFLVTLPMIHYRGHNWFGHGCKLLSGFYHTG 120

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DB 61 QYKRAKNTSTIYLMLAISDLLEFTLPFWISYQAKTDWVGNACKVLSGYTYGLISE 120
QY 121 IFFIILLTIDRYLAIVHAFALRARTVFGVITSIVTWGLAVLAALPEFIYETEELPEE 180
DB 121 IFFIILLTIDRYLAIVHAFALRARTVFGVITSIIIVLAILASLPGIYFAKTQWEITH 180
QY 181 TLCSALYEDPDVYSRHRHTLMTIFCLVPLLVNAICYTGIIKLLRCPSSKKYKAIRL 240
DB 181 RTCSLHPHESKOEKRLQALKNLGLVPLLVAVICYTGIIKLLRPNKPKSKAVL 240
QY 241 IFVIAVFEIEMTPYNAVALLSYOSILFGNDCERSKHLDMVLTVEVAYSHCMPYI 300
DB 241 IFVIMIIFFELMTYFNLTLLISVRODFLETYCCEGROLDLAIQVTEMAIATYHCCVNPYI 300
QY 301 YAFVGERFRKYLHFFHRLMLHGRYIPFLPSEKLETSVSPSTABEELSVF 355
DB 301 YAFVGERFRKHLRLQFHRRAVAVLKMPLFSVDBLERASSVSPSTGEHEVSNAGF 355
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RESULT 7

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Q9JLY8 PRELIMINARY: PRT; 355 AA.
AC Q9JLY8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Macrophage inflammatory protein-1 alpha receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD;
RX MEDLINE=20555330; PubMed=11091494;
RA Waller A., Nayee P., Czaplowski L.G.;
RT Identification and characterization of a rat macrophage inflammatory
RT protein-1 alpha receptor.
RL J. Hematother. Stem Cell Res. 9:703-710(2000).
DR EMBL; AF119381; AAF34340.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 355 AA; 40838 MW; 2FEB8661D1E6E075 CRC64;
```

Query Match 60.2%; Score 1115.5; DB 11; Length 355;
Best Local Similarity 58.6%; Pred. No. 2e-90; Indels 1; Gaps 1;
Matches 202; Conservative 66; Mismatches 76;

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QY 9 ETEFGTSTYD-DVGLCEKADTRALMAQVPPVLSYFTVGLGNVVMILIKYRLAI 67
DB 8 EYPTTTEYDGDSPQCKTVARAGAGLLPLYSFVLIGVGNLIVLVMQHRRLQS 67
QY 68 MTNITLMLAISDLLEFTLPFWIHVYRGHNVFGHGMKLLSGYHTGLYSEIFPI 127
DB 68 MTSITLFLNLAASDLVFLFTLPFWIDYKLDNMVFGDAMCKLLSGFYTLGLYSEIFPI 127
QY 128 TIDRYLAIVHAFALRARTVFGVITSIVTWGLAVLAALPEFIYETEELPEETLCSALY 187
DB 128 TIDRYLAIVHAFALRARTVFGVITSIIIVLAILASLPGIYFAKTQWEITH 180
QY 188 PEDVYSRHRHTLMTIFCLVPLLVNAICYTGIIKLLRCPSSKKYKAIRLIFVIMAY 247
DB 188 PDESILKTKRFOALKNLGLILPLVMICYAGIIRILRPNKPKAKAVLIRAITLL 247
QY 248 FFIFETPYNAVALLSYOSILFGNDCERSKHLDMVLTVEVAYSHCMPYIYAFVGER 307
DB 248 FFLMTPYNLTIVVSAFQDVLEFTNOCBOSKOLDLAIQVTEVLAIVYHCCVNPITIVVGER 307
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QY 308 FRKYLRHFRHLMLHGRYIPFLPSEKLETSVSPSTABEELS 352
DB 308 FRKYLRQLEQRHVAIPLAKMLPFSVDLERASSVSPSTGEHELS 352
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RESULT 8

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Q91VP9 PRELIMINARY: PRT; 355 AA.
AC Q91VP9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chemokine (C-C) receptor 1.
GN CMKRL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011092; AAH1092.1;
DR MGD; MGI:104618; Cmkpr1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1;
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 355 AA; 40894 MW; 41B0D566A56BC4F7 CRC64;
```

Query Match 60.2%; Score 1115.5; DB 11; Length 355;
Best Local Similarity 58.7%; Pred. No. 2e-90;
Matches 206; Conservative 62; Mismatches 82; Indels 1; Gaps 1;

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QY 6 DVEFGTSTYD-DVGLCEKADTRALMAQVPPVLSYFTVGLGNVVMILIKYRLAI 64
DB 5 DTEATPTTEYDGDSPQCKTVARAGAGLLPLYSFVLIGVGNLIVLVMQHRRL 64
QY 65 IRTNITLMLAISDLLEFTLPFWIHVYRGHNVFGHGMKLLSGYHTGLYSEIFPI 124
DB 65 IQSMSTIYFLNLAASDLVFLFTLPFWIDYKLDNMVFGDAMCKLLSGFYTLGLYSEIFPI 124
QY 125 ILLTIDRYLAIVHAFALRARTVFGVITSIVTWGLAVLAALPEFIYETEELPEETLCS 184
DB 125 ILLTIDRYLAIVHAFALRARTVFGVITSIIIVLAILASLPGIYFAKTQWEITH 180
QY 185 ALYEDPDVYSRHRHTLMTIFCLVPLLVNAICYTGIIKLLRCPSSKKYKAIRLIFVIMAY 244
DB 185 PHFPYKSLQMRFOALKNLGLILPLVMICYAGIIRILRPNKPKAKAVLIRAITLL 244
QY 245 MAVFIFETPYNAVALLSYOSILFGNDCERSKHLDMVLTVEVAYSHCMPYIYAFV 304
DB 245 TLFLFTLPFWISVSAFQDVLEFTNOCBOSKOLDLAIQVTEVLAIVYHCCVNPITIVV 304
QY 305 GERFRKYLHFFHRLMLHGRYIPFLPSEKLETSVSPSTABEELSVF 355
DB 305 GERFRKYLRLQFHRRAVAVLKMPLFSVDBLERASSVSPSTGEHELSAGF 355
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RESULT 9

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Q89609 PRELIMINARY: PRT; 383 AA.
AC Q89609;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE G protein-coupled receptor.
OS Equine herpesvirus type 2 (strain 86/87) (EHV-2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxId=82831;
```

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9302501; PubMed-7783207;
RA Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
RT "The DNA sequence of equine herpesvirus 2."
RL J. Mol. Biol. 249:520-528(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Telford E.A.R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U20824; AAC13866.1; -
DR EMBL: U20824; AAC13788.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
SQ SEQUENCE 383 AA; 43667 MW; 0C65C53EAF539F72 CRC64;

Query Match 51.7%; Score 958.5; DB 12; Length 383;
Best Local Similarity 50.6%; Pred. No. 1.5e-76;
Matches 183; Conservative 63; Mismatches 87; Indels 29; Gaps 3;

QY 2 TTSIDVETFGTTS-----YYDDV-----GLCEKADTRALM 33
DB 12 TTSIDVETFGTTS-----YYDDV-----GLCEKADTRALM 71
QY 34 AGVPPPLSLVETVGLGNVVMILIKYRLRIMTYLNLAISDLLEVLTPFWIHY 93
DB 72 AGVPPALYLLVLEGLGNLIVVIVRYMKIKMLNMLNLAISDLLEVLTPFWIHY 131
QY 94 V-RGNHNVFGHGMCKLISGFYHNGYSEIFPIILLTDRIYAIYHAPALBARVTVGVI 152
DB 132 IGMHDTFGISLCKLRGVCYMSLYSOVFCILLTVDRYLAIVYAVTALREFRYTGIV 191
QY 153 TSVITWGLAVLALPEEFYETELFEETLCSALYPERVYSNRHFTLMTFCLVPL 212
DB 192 TCVCWTWLAGLISLPEFFGHODNGRVOCDPRYEMSTWWRRAHAKYIMLSLILPL 251
QY 213 LVNAICTYGIITKTLRCPSSKKRYKARILYIVAVFPIEMTPYVAILSSYOSILFGND 272
DB 252 LIMAVCYVYIIRLLRRPSKKRYKARILYIVAVFEMTPYVAILSSYOSILFGND 311
QY 273 CERSKHLDVNLVTEVAYSHCCNRPYIYAVGGERFRKYLAHFHRHLMILGRIYPLP 332
DB 312 CALSSNLDMLLIRTYAHTHCINPIYIAVGEKFRHLHFHTYAYAILCRYIPLS 371
QY 333 SE 334
DB 372 GD 373

RESULT 10
Q9TQ03 PRELIMINARY; PRT; 339 AA.
AC Q9TQ03;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnridae; Lemur.
OX NCBI_TaxID=9447;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162011; AAD47766.1; -
DR EMBL: AF162008; AAD47763.1; -

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DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
RW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38712 MW; 8A2DD074093A56AE CRC64;

Query Match 51.7%; Score 958; DB 6; Length 339;
Best Local Similarity 55.8%; Pred. No. 1.5e-76;
Matches 188; Conservative 55; Mismatches 88; Indels 6; Gaps 5;

QY 17 YD-DVGLT--CEKADTRALMAQFVPLSLVETVGLGNVVMILIKYRLRIMTYL 73
DB 3 YDIDYGLSEPOKIDVRIKIAQLPLSLVETVGLGNVVMILIKYRLRIMTYL 62
QY 74 LNLAISDLLEVLTPFWIHYRGHNVFGHGMCKLISGFYHNGYSEIFPIILLTDRIYL 133
DB 63 LNLAISDLLEVLTPFWIHYRGHNVFGHGMCKLISGFYHNGYSEIFPIILLTDRIYL 121
QY 134 AIVHAFALRARTVETGVTISITVGLVLAALPEEFYETELFEETLCSALYPERIVY 193
DB 122 AIVHAFALRARTVETGVTISITVGLVLAALPEEFYETELFEETLCSALYPERIVY 181
QY 194 SWRHEHRLMTFICLVPLVLAIAICTYGIITKTLRCPSSKKRYKARILYIVAVFPIEM 252
DB 182 FKNRQVQKMLVGLVLEPLLVINVCYSGILTKTLRCRERKRHRKARILYIVAVFPIEM 241
QY 253 TPYVAVAILSSYOSILFGNDERSKHLDVNLVTEVAYSHCCNRPYIYAVGGERFRKYL 312
DB 242 APYVAVAILSSYOSILFGNDERSKHLDVNLVTEVAYSHCCNRPYIYAVGGERFRKYI 301
QY 313 RHFHRHLMILGRIYPLPSEKLERTSSV-SPSTAE 348
DB 302 LDFPRKHIAKFPCKCQPFQREAVPERGSSVYTRISGE 338

RESULT 11
Q9TQ03 PRELIMINARY; PRT; 339 AA.
AC Q9TQ03;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Lemur variegatus (Ruffed lemur) (Varecia variegata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnridae; Varecia.
OX NCBI_TaxID=9455;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162014; AAD47769.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
RW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38713 MW; 77DCE451AA3A4CB6 CRC64;

Query Match 51.6%; Score 956; DB 6; Length 339;
Best Local Similarity 55.8%; Pred. No. 2.2e-76;
Matches 188; Conservative 54; Mismatches 89; Indels 6; Gaps 5;

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QY	17	YD-DVGLL--CEBADFALMAQCEVPPPLYSIVSEFVGLGVNVMALIKRRLRIMNTYL	73
Db	3	YDIDYGLSEPCQKIDVKRIQAQGLLPPLYSIVSEFGLVGNMLVYLDLNOCKKLKSMYDYL	62
QY	74	LNLAISLLELLPPIHIVYRGHNHNVFGHGCKMLSGYRHGYSIEIPFILLTDRL	13
Db	63	LNLAISLLELLPVPFAHAAA--QMDPGMTMQQLTGTFYIGFESGVFFILLTDRL	12
QY	134	AIYHAYEALBARTVTEGVITSIYTWGLAVLAALPEPIFYETEHELBETLCSALYPEDYV	19
Db	122	AIYHAYEALBARTVTEGVITSGVTWVAVALSLPGIILFRSQEGELRYTCSLHPRSOYQ	18
QY	194	SMRHFHLRMTICLVPLPLVMAICTGIIKTLTRC--PSKKRKATRLFEVMAVEFIW	25
Db	182	FMKNFQLKRLVGLVPLPLVMTYICSGILKTLTRCERTEKKRAVRLFAIMYIFELW	24
QY	253	TPNVAVALLSYOSILEGNDCKERSKHLDMLTEVIAVSHCCMNPVIAIVGGERKYL	31
Db	242	APNVAIVALLMTPEFEGFLDNCSSSNGIDQAMQUTETLIGMTHCCINPVYAFVGEKRRYI	30
QY	313	RHFPHRLHMLGRVIFELPSEKLETRSSV--SPSTAE	348
Db	302	LDPFHKHIAIRPCKCPVQREVPREKGSSTVYTSTGE	338

[illegible][illegible]

ID	097975	PRELIMINARY;	PRT;	352 AA.
AC	097975			
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
DE		C-C chemokine receptor type 5.		
GN		CCR5.		
OS		Macaca arctoides (Stump-tailed macaque), and		
OS		Macaca assamensis (Assam's macaque) (Assam's monkey).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC		Cercopithecinae; Macaca.		
OX		NCBI_TaxID=9540, 9551;		
RN		[1]		
RP		SEQUENCE FROM N.A.		
RA		Zhang Y.-W., Zhang Y.-P.;		
RT		"Sequence evolution of chemokine receptor CCR5 gene in primates."		
RL		Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.		
DR		EMBL; AF075450; AAD19862.1; -		
DR		EMBL; AF075449; AAD19861.1; -		
DR		InterPro; IPR000276; GPCR_Rhodopsn.		
DR		Pfam; PF00001; 7tm1.1; 1.		
DR		PRINTS; PR00237; GPCR_RHODOPSIN.		
DR		PROSITE; PS00237; G_PROTEIN_RECPT_FL1; UNKNOWN_1.		
DR		PROSITE; PS50262; G_PROTEIN_RECPT_FL2; 1.		
DR		Receptor.		
SO		SEQUENCE		
		352 AA; 40521 MW; 5F276C85909FACB2 CRC64; .		
		51.4%; Score 953.5; DB 6; Length 352;		
		Best Local Similarity 54.8%; Pred. No. 3,8e-76;		
		Matches 182; Conservative 58; Mismatches 89; Indels 3; Gaps 3		
OY	24	CEKADTRALMAQFPPPLISLVFTVGLGNVVVMIILIKYRLRLMTNTYLLNLAIISDLF	83	
DB	20	COKINVKQIARLRPLPLYSIVFEGVGNILVLLILCKRUKSWTDIYLLNLAIISDLF	79	
OY	84	LVTLDFWVHHYGRGHNVVGHCKMCKLSGFYHTGLSELPFILLTDRIYLVAVHFAIR	143	
DB	80	LLTVPEFMAHYAA-OMDFGNMCKQLTSLYELGFSGIFFIILLIDRIYLVAVHFAIR	138	
OY	144	ARTVTFGVTISVTVGLVLAALPEFIYETPELFEERLCSALYPEDPVYSNRHPTLRM	203	
DB	139	ARTVTFGVTVITVWVAVFASLPGLITTRSGRBSLHTCCSHFYSQYQFKNKQTLRM	198	
OY	204	TIFCVLPFLVMAICCTGIIKTLNCPK-KKKYKARILFLVMAVETFTPYNAAILLS	262	
DB	199	VILGVLPFLVMAVICYSGIILKTLNCRNKKRHRVRLITFTIMYIFLFMAFYNVLLN	258	
OY	263	SYGSILFSGNDCRSKHLDLVNLVTEVIAVSHCCMPVITVAFGEGRFRYLRHFFRHLLM	322	
DB	259	TTFEERFGNLCSSNRDLDAQVETELGNTHCICINPIIYAFVGEKFRNVLVTFQKILAK	318	
OY	323	HLGRYIFLPSEKLERTSSV-SPTAAPELST	353	
DB	319	RFCRCOSIFQGEAPERRASSVYTRSAEQEISV	350	

01-MAY-2000 (Tremblrel. 13, Created)
01-MAY-2000 (Tremblrel. 13, Last sequence update)
01-JUN-2001 (Tremblrel. 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
CCRS.
OS Lemur variegatus (Ruffed lemur) (Varecia variegata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Varecia.
NCBI_TaxID=9455;
RN
RP STRAIN-52;
RA Kunstan K., Yoder A., Korb B., Oprendeck J., Stanton J., Agy M.,
Shtabara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF162009; AAD47764.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR Receptor.
KW Receptor.
FT NON_TER
SQ SEQUENCE 339 AA; 38664 MW; B53CFE4F6B09E1A CRC64;
Query Match 51.4%; Score 953; DB 6; Length 339;
Best Local Similarity 55.8%; Pred. No. 4.1e-76;
Matches 188; Conservative 54; Mismatches 89; Indels 6; Gaps 5;
QY 17 YD-DVGL--CEKADTRALMAQFVPLYSLVFTVGLGNVVMILIKYRLRMTNTIYL 73
DB 3 YDIDGSEPCQKIDKVRIRIAQQLPLYSVIFGLGNMILVLLINCKRILKSMTDIYL 62
QY 74 LNLASDLFLVLPFEMHVRGNHVRGCMCKLSGFEYTGIXSEFFIILLITDRIYL 133
DB 63 LNLASDLFLVLPFEMHVRGNHVRGCMCKLSGFEYTGIXSEFFIILLITDRIYL 121
QY 134 AIVAVPALRAVTFVGVITSIYVGLAVLAALPEFIEETEELFEETLCSALYPEDTVY 193
DB 122 AIVAVPALRAVTFVGVITSIYVGLAVLAALPEFIEETEELFEETLCSALYPEDTVY 181
QY 194 SMRFHRLKMTIFCLVPLVMAICYGIITLLRCP5-KKRYAIRLIFYIMAVFLEW 252
DB 182 FMKFOPLKMLVGLVPLVMAICYGIITLLRCP5-KKRYAIRLIFYIMAVFLEW 241
QY 253 TPYVAVILSSYOSILRGNDCERSKHLDVLAALPEFIEETEELFEETLCSALYPEDTVY 312
DB 242 APYVAVILSSYOSILRGNDCERSKHLDVLAALPEFIEETEELFEETLCSALYPEDTVY 301
QY 313 RHFFHRLMLHGRYIPFLPSEKLEKRTSSV-SPSTAE 348
DB 302 LDFFHRLMLHGRYIPFLPSEKLEKRTSSV-SPSTAE 338
RESULT 15
Q9TV48 PRELIMINARY; PRT; 352 AA.
AC Q9TV48;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CC chemokine receptor type 5.
GN CCR5.
OS Cercopithecus acaulus (black-cheeked white-nosed monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
NCBI_TaxID=36223;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-52;

MEMLINE-99335215; PubMed-10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with HIV
carrier status in African nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-52;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
Georges-Courbot M.C., Barre-Sinoussi F., Fomsgaard A.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF035216; AAD44009.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40650 MW; 7906236AA3945266 CRC64;
Query Match 51.4%; Score 952.5; DB 6; Length 352;
Best Local Similarity 54.5%; Pred. No. 4.7e-76;
Matches 181; Conservative 58; Mismatches 90; Indels 3; Gaps 3;
QY 24 CEKADTRALMAQFVPLYSLVFTVGLGNVVMILIKYRLRMTNTIYLNLASDLLE 83
DB 20 COKINVKQIAARLLPLYSVIFGVGNILVLLINCKRILKSMTDIYLNLASDLLE 79
QY 84 LVLPLFVHVRGNHVRGCMCKLSGFEYTGIXSEFFIILLITDRIYLAIVAVPALR 143
DB 80 LVLPLFVHVRGNHVRGCMCKLSGFEYTGIXSEFFIILLITDRIYLAIVAVPALR 138
QY 144 ARTVFGVITSIYVGLAVLAALPEFIEETEELFEETLCSALYPEDTVYSMRHPTLRM 203
DB 139 ARTVFGVITSIYVGLAVLAALPEFIEETEELFEETLCSALYPEDTVYSMRHPTLRM 198
QY 204 TIFCLVPLVMAICYGIITLLRCP5-KKRYAIRLIFYIMAVFLEWTPYVAVILS 262
DB 199 TIFCLVPLVMAICYGIITLLRCP5-KKRYAIRLIFYIMAVFLEWTPYVAVILS 258
QY 263 SYOSILRGNDCERSKHLDVLAALPEFIEETEELFEETLCSALYPEDTVYSMRHPTLRM 322
DB 259 TFOEPFGILNCCSSNRILDAQAVETLMTCCINPIIYAVGEXRNYLLVFOKHIAK 318
QY 323 HLGRYIPFLPSEKLEKRTSSV-SPSTAEDELSI 353
DB 319 RFCKCCSIFQOEAPERBASVYTRSTGEDEISV 350

Search completed: June 27, 2003, 18:14:28
Job time : 84 secs

